

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	33396	XU.INV.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:05
L2	10469	\$atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:05
L3	35397	digoxin or digitoxin or ouabain OR GLYCOSIDE\$2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:06
L5	11	1 AND 2 AND 3	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:07
L6	336356	(ANTIBOD\$3 OR IMMUNOGLOBULIN\$4 OR IMMUN\$2GLOBULIN\$4 OR GAMMA\$1GLOBULIN\$4 OR MAB\$10 OR Fab\$1 OR fab\$4sub\$10 OR hybridoma\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:14
L7	1283	2 AND 3 AND 6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:14
L8	1319	anti-na\$12 OR anti-NKA	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:15
L9	20	7 AND 8	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:15

(FILE 'HOME' ENTERED AT 16:16:41 ON 08 MAY 2007)

FILE 'MEDLINE, CAPLUS, EMBASE, BIOSIS' ENTERED AT 16:17:21 ON 08 MAY 2007

L1	117 S XU/AU
L2	1 S RSATEEEPPNDD
L3	0 S L1 AND L2
L4	72922 S INOTROP?
L5	0 S L4 AND L1
L6	5224 S XU K?/AU
L7	38 S L6 AND L4

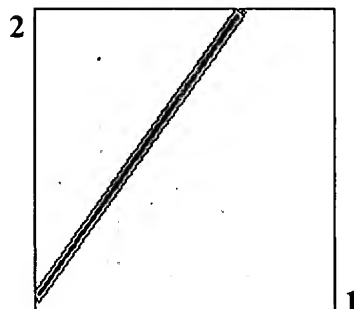
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

Matrix: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter: ☐ View option:
 Masking character option: Masking color option:
☐ Show CDS translation

Sequence 1: lcl|AAA416701_Rat_NaK
 Length = 1023 (1 .. 1023)

Sequence 2: lcl|SEQ_ID_NO:745
 Length = 750 (1 .. 750)

Rosen et al.



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1381 bits (3575), Expect = 0.0, Method: Composition-based stats.
 Identities = 673/712 (94%), Positives = 689/712 (96%), Gaps = 5/712 (0%)

Query	1	MGKGVGRDKYEPAAVSEHGDKKSKKAKKERDMDLKKKEVSMDDHKLSLDELHRKYGTDLS	60
		MGKGVGRDKYEPAAVSE GDKK KK KK+RDMDELKKKEVSMDDHKLSLDELHRKYGTDLS	
Sbjct	37	MGKGVGRDKYEPAAVSEQGDKKGGKGGKDRDMDLKKKEVSMDDHKLSLDELHRKYGTDLS	96
Query	61	RGLTPARPVEILARDGPNALTTPPTTPEWVKFCRQLFGGFSMLLWIGAILCFLAYGIRSA	120
		RGLT AR EILARDGPNALTTPPTTPEW+KFCRQLFGGFSMLLWIGAILCFLAY II++A	
Sbjct	97	RGLTSARAAEILARDGPNALTTPPTTPEWIKFCRQLFGGFSMLLWIGAILCFLAYSIOAA	156
Query	121	TEEEPPNDLLYLGVVLSAVVIITGCFSSYYQEA KSSKIMESFKNMVPQQALVIRNEEKMSI	180
		TEEEP. ND+LYLGVVLSAVVIITGCFSSYYQEA KSSKIMESFKNMVPQQALVIRN EKMSI	
Sbjct	157	TEEEPQNDNLYLGVVLSAVVIITGCFSSYYQEA KSSKIMESFKNMVPQQALVIRNGEKMSI	216
Query	181	NAEDVVVVDLVEVKGGDRIPADLR IISANGCKVDNSSLTGESEPQTRSPDFTNENPLETR	240
		NAE+VVV DLVEVKGGDRIPADLR IISANGCKVDNSSLTGESEPQTRSPDFTNENPLETR	
Sbjct	217	NAEEVVVGDLVEVKGGDRIPADLR IISANGCKVDNSSLTGESEPQTRSPDFTNENPLETR	276
Query	241	NIAFFSTNCVEGTARGIVVYTGDRITVMGRIATLASGLEGGQTPIAEIEHFIHLITGVAV	300
		NIAFFSTNCVEGTARGIVVYTGDRITVMGRIATLASGLEGGQTPIA EIEHFIH+ITGVAV	
Sbjct	277	NIAFFSTNCVEGTARGIVVYTGDRITVMGRIATLASGLEGGQTPIAAEIEHFIHIITGVAV	336
Query	301	FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEVLLATVTVCLTLTAKRMARKNCLVKN	360

Sbjct	337	FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPE LLATVTVCLTLTAKRMARKNCLVKN	396
Query	361	LEAVETLGSTSTICSDKTGTLTQNRMTVAHMFWDNQIHEADTTENQSGVSFDKTSATWFA	420
Sbjct	397	LEAVETLGSTSTICSDKTGTLTQNRMTVAHMFWDNQIHEADTTENQSGVSFDKTSATWLA	456
Query	421	LSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIEVCCGSVMEMREKYTKIVEI	480
Sbjct	457	LSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIE+CCGSV EMRE+Y KIVEI	516
Query	481	PFNSTNKYQLSIHKNPNASEPKHLLVMKGAPERILDRCSSILLHGKEQPLDEELKDAFQN	540
Sbjct	517	PFNSTNKYQLSIHKNPNTSEPQHLLVMKGAPERILDRCSSILLHGKEQPLDEELKDAFQN	576
Query	541	AYLELGGLGERVLGFCHLLLPDEQFPEGFQFDTDEVNFPVDNLCFVGLISMIDPPRAAVP	600
Sbjct	577	AYLELGGLGERVLGFCHL LPDEQFPEGFQFDTD+VNFP+DNLCFVGLISMIDPPRAAVP	636
Query	601	DAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAARLNIPVNQVNPRDA	660
Sbjct	637	DAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAARLNIPV+QVNPRDA	696
Query	661	KACVVHGSDLKDMTSEELDDILRYHTEIVFARTSPQQKLIIVE-----GCQR	707
Sbjct	697	KACVVHGSDLKDMTSE+LDDIL+YHTEIVFA+TSPQQKLIIVE GC R	748

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

4 pages of
aligned
seqs.

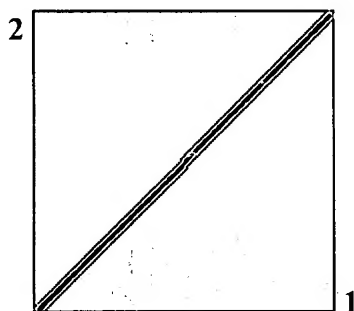
28
5-7-07

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **0** expect: **10.000** wordsize: **3** Filter ☐ View option **Standard**
Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: lcl|rat_NaK Genbank Acc # AAA41671
Length = 1023 (1 .. 1023)

Sequence 2: lcl|human_NaK Genbank Acc # NP_000692
Length = 1023 (1 .. 1023)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Sequence alignment visualization showing two horizontal bars representing the sequences. The top bar is labeled 'Query' and the bottom bar is labeled 'Sbjct'. The bars are aligned, indicating a high degree of similarity between the two sequences.

Score = 2051 bits (5315), Expect = 0.0, Method: Composition-based stats.
Identities = 985/1023 (96%), Positives = 1001/1023 (97%), Gaps = 0/1023 (0%)

Query	1	MGKGVGRDKYEPAAVSEHGDKSKKAKKERDMDLKKKEVSMDDHKLSLDELHRKYGTDLS	60
		MGKGVGRDKYEPAAVSE GDKK KK KK+RDMDELKKKEVSMDDHKLSLDELHRKYGTDLS	
Sbjct	1	MGKGVGRDKYEPAAVSEQGDKKGKKGKDRDMDLKKKEVSMDDHKLSLDELHRKYGTDLS	60
Query	61	RGLTPARPVEILARDGPNALTPPPTTPEWVKFCRQLFGGFSMLLWIGAILCFLAYGIRSA	120
		RGLT AR EILARDGPNALTPPPTTPEW+KFCRQLFGGFSMLLWIGAILCFLAY I++A	
Sbjct	61	RGLTSARAAEILARDGPNALTPPPTTPEWIKFCRQLFGGFSMLLWIGAILCFLAYSIDAA	120
Query	121	TEEEPPNDDLYLGVVLSAVVIITGCFSYYQEAKSSKIMESFKNMVPPQALVIRNEEKMSI	180
		TEEEP ND+LYLGVVLSAVVIITGCFSYYQEAKSSKIMESFKNMVPPQALVIRN EKMSI	
Sbjct	121	TEEEPQNDNLYLGVVLSAVVIITGCFSYYQEAKSSKIMESFKNMVPPQALVIRNGEKMSI	180
Query	181	NAEDVVVVDLVEVKGGDRIPADLRIISANGCKVDNSSLTGESEPPQTRSPDFTNENPLETR	240
		NAE+VVV DLVEVKGGDRIPADLRIISANGCKVDNSSLTGESEPPQTRSPDFTNENPLETR	
Sbjct	181	NAEEVVVGDLVEVKGGDRIPADLRIISANGCKVDNSSLTGESEPPQTRSPDFTNENPLETR	240
Query	241	NIAFFSTNCVEGTARGIVVYTGDRVTMGRIATLASGLEGGQTPIAEEIEHFIHLITGVAV	300
		NIAFFSTNCVEGTARGIVVYTGDRVTMGRIATLASGLEGGQTPIA EIEHFIH+ITGVAV	
Sbjct	241	NIAFFSTNCVEGTARGIVVYTGDRVTMGRIATLASGLEGGQTPIAEEIEHFIHIITGVAV	300
Query	301	FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEVLLATVTVCLTLTAKRMARKNCLVKN	360

Sbjct	301	FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPE LLATVTVCLTLTAKRMARKNCLVKN FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKN	360
Query	361	LEAVETLGSTSTICSDBKTGTLTQNRMTVAHMMWFDNQIHEADTTENQSGVSFDKTSATWFA LEAVETLGSTSTICSDBKTGTLTQNRMTVAHMMWFDNQIHEADTTENQSGVSFDKTSATW A	420
Sbjct	361	LEAVETLGSTSTICSDBKTGTLTQNRMTVAHMMWFDNQIHEADTTENQSGVSFDKTSATWLA	420
Query	421	LSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIEVCCGSVMEMREKYTKIVEI LSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIE+CCGSV EMRE+Y KIVEI	480
Sbjct	421	LSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIELCCGSVKEMRERYAKIVEI	480
Query	481	PFNSTNKYQLSIHKPNPASEPKHLLVMKGAPERILDRCSSILLHGKEQPLDEELKDAFQN PFNSTNKYQLSIHKPNP SEP+HLLVMKGAPERILDRCSSILLHGKEQPLDEELKDAFQN	540
Sbjct	481	PFNSTNKYQLSIHKPNPTSEPQHLLVMKGAPERILDRCSSILLHGKEQPLDEELKDAFQN	540
Query	541	AYLELGGGLGERVLGFCHLLLPDEQFPEGFQFDTDEVNFPVDNLCFVGLISMIDPPRAAVP AYLELGGGLGERVLGFCHL LPDEQFPEGFQFDTD+VNFP+DNLCFVGLISMIDPPRAAVP	600
Sbjct	541	AYLELGGGLGERVLGFCHLFLPDEQFPEGFQFDTDDVNFPIDNLCFVGLISMIDPPRAAVP	600
Query	601	DAVGKCRSAGIKVIMVTGDHPITAKAIAGVGIIISEGNETVEDIAARLNIPVNQVNPRDA DAVGKCRSAGIKVIMVTGDHPITAKAIAGVGIIISEGNETVEDIAARLNIPV+QVNPRDA	660
Sbjct	601	DAVGKCRSAGIKVIMVTGDHPITAKAIAGVGIIISEGNETVEDIAARLNIPVSQVNPRDA	660
Query	661	KACVVHGSDDLKDMTSEELDDILRYHTEIVFARTSPQQLIIVEGCQRQGAIVAVTGDGVN KACVVHGSDDLKDMTSE+LDDIL+YHTEIVFARTSPQQLIIVEGCQRQGAIVAVTGDGVN	720
Sbjct	661	KACVVHGSDDLKDMTSEQLDDILKYHTEIVFARTSPQQLIIVEGCQRQGAIVAVTGDGVN	720
Query	721	DSPALKKADIGVAMGIVGSDVSKQAADMILLDDNFASIVTGVEEGRILFDNLKKSIAAYTL DSPALKKADIGVAMGI GSDVSKQAADMILLDDNFASIVTGVEEGRILFDNLKKSIAAYTL	780
Sbjct	721	DSPALKKADIGVAMGIAGSDVSKQAADMILLDDNFASIVTGVEEGRILFDNLKKSIAAYTL	780
Query	781	TSNIPEITPFLIFIIANIPLPLGTVTILCIDLGTMVPAISLAYEQAESDIMKRQPRNPK TSNIPEITPFLIFIIANIPLPLGTVTILCIDLGTMVPAISLAYEQAESDIMKRQPRNPK	840
Sbjct	781	TSNIPEITPFLIFIIANIPLPLGTVTILCIDLGTMVPAISLAYEQAESDIMKRQPRNPK	840
Query	841	TDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLPFHLLGIRETWDDRWINDEV TDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLP HLLG+R WDDRWINDEV	900
Sbjct	841	TDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLPIHLLGLRVDWDDRWINDEV	900
Query	901	SYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFE SYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFE	960
Sbjct	901	SYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFE	960
Query	961	ETALAFLSYCPMGGAALRMYPLKPTWWFCAFPYSLIFVYDEVKLIIRRRPGGWVEKE ETALAFLSYCPMG ALRMYPLKPTWWFCAFPYSLIFVYDEVKLIIRRRPGGWVEKE	1020
Sbjct	961	ETALAFLSYCPMGVALRMYPLKPTWWFCAFPYSLIFVYDEVKLIIRRRPGGWVEKE	1020
Query	1021	TTY 1023 TTY	
Sbjct	1021	TTY 1023	

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.